

GenCore version 4.5						
Copyright (c) 1993 - 2000 Compugen Ltd.						
protein - protein search, using sw model						
run on:	February 11, 2002, 13:31:18 ;	Search time 13.29 Seconds				
	(without alignments)					
	899.378 Million cell	updates/sec				
title:	US-09-553-431-2					
perfect score:	1654					
sequence:	1 MASLRLFSTNHQSLLPSSL.....KAVMVEEPPKKRGFFSFGGG 326					
scoring table:	BLOSUM62					
Gapop:	10.0 , Gapext: 0.5					
searched:	100059 seqs, 36664827 residues					
total number of hits satisfying chosen parameters:	100059					
minimum DB seq length:	0					
maximum DB seq length:	2000000000					
post-processing:	Maximum Match 0%					
	Maximum Match 100%					
	Lasting first 45 summaries					
database:	SwissProt_39;*					
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.						
SUMMARIES						
result No.	Score	Query Match Length	DB ID	Description		
1	799.5	483	1 MIND_NESVLI	Q9mm5 mesostigma		
2	792	479	1 MIND_CHLVU	P56346 chlorella v		
3	694.5	420	1 MIND_GIITH	078436 chlorella v		
4	643	389	1 MIND_SYNY3	Q55900 synechocystis		
5	523	311	1 MIND_BACSU	P10164 bacillus su		
6	506.5	306	1 MIND_HBLPY	025058 helicobacte		
7	500.5	303	1 MIND_HELPJ	09zna8 helicobacte		
8	479.5	290	1 MIND_ESCOLI	P18197 escherichia		
9	475.5	287	1 MIND_THEMEA	Q9x213 thermotoga		
10	460	278	1 MIND_BUCAI	P57411 buchnera ap		
11	300	181	1 MIND_HBLPY	Q57967 methanococcus		
12	242	146	1 Y169_METJA	Q57653 methanococcus		
13	214	129	1 YLXH_BACSU	P40742 bacillus su		
14	-	213	1 MRP_SYN3	P53225 synchocystis		
15	211	128	1 MRP_AQUAE	066946 aquifex aeo		
16	209	126	1 MRP_HELPJ	09znm5 helicobacte		
17	206	125	1 MRP_HELPJ	024993 helicobacte		
18	197.5	119	1 MRP_DICRA	Q9rvn9 denococcus		
19	193.5	117	1 Y949_PYRHO	058667 pyrococcus		
20	191	115	1 Y283_METJA	P53731 methanococcus		
21	190	115	1 MRP_MCTU	033225 mycobacteri		
22	183.5	111	1 Y685_METJA	058098 methanococcus		
23	183	111	1 SOJ_BACSU	P37522 bacillus su		
24	181	109	1 YCAB_SFESR	P72190 pseudomonas		
25	177.5	107	1 MRP_MCYCLE	P53392 mycobacteri		
26	173.5	105	1 NUB2_HUMAN	Q9y52 hono sapient		
27	173.5	105	1 MRP_ECOLI	P21590 escherichia		
28	165	100	1 Y823_METJA	058223 methanococcus		
29	164.5	99	1 PARA_CAUR	058189 rhabdobacter		
30	164	99	1 NUB2_MOUSE	09r061 mus musculus		
31	161	97	1 Y924_METJA	058334 methanococcus		
32	160	97	1 BCHL_BHORU	Q9zg15 rhabdobi		
33	153.5	93	1 BCHL_BHORU	Q9zg15 rhabdobi		

RESULT	1	MIND_MESVI	STANDARD;	PRT;	286 AA.
ID	MIND_MESVI				
AC	Q9MUM5;				
DT	20-AUG-2001	(Rel. 40, Created)			
DT	20-AUG-2001	(Rel. 40, Last sequence update)			
DT	20-AUG-2001	(Rel. 40, Last annotation update)			
DE	PUTATIVE SEPTIN SITE-DETERMINING PROTEIN MIND.				
GN	MIND.				
OS	Mesostigma viride.				
OG	Chloroplast.				
OC	Eukaryota; Viridiplantae; Streptophyta; Mesostigmatophyceae;				
OC	Mesostigmatales; Mesostigmataceae; Mesostigma.				
OX	NCBI_TAXID=41882;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=NIES-296;				
RX	MEDLINE=20150907; PubMed=10688199;				
RA	Leinonen C., Ots C., Turmel M.;				
RT	"Ancient chloroplast genome in Mesostigma viride reveals an early branch of green plant evolution."				
RL	Nature 03:649-652 (2000).				
CC	- ! - FUNCTION: ATPase required for the correct placement of the CC DIVISION SITE (BY SIMILARITY).				
CC	- ! - SIMILARITY: BELONGS TO THE PARA FAMILY. MIND SUBFAMILY.				
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CC	-----				
DR	EMBL; AF166114; AAF41873.1; -.				
DR	InterPro; IPR000707; ParaA.				
DR	Pfam; PF00591; ParaA_1.				
KW	Cell division; Septation; ATP-binding; Chloroplast.				
FT	NP-BIND	25	32	ATP (POTENTIAL).	
SQ	SEQUENCE	286 AA;	31627 MW;	25D8B8FB2258E3F9 CRC64;	
Query Match	48/38;	Score 799.5;	DB 1;	Length 286;	
Best Local Similarity	60.4%	Pred. No. 1.9e-57			
Matches	166; Conservative	39; Mismatches	61; Indels	9; Gaps	4
Qy	46 QFNKRPELAGET-PRIVVITSGKGVGKTTTANVGLSLARYGFSVVAAIDADLGFLRNLDL 104				
Db	4 QINKDEKKNSTDTRITVITGKGKGKTTTANLGMISIARIGYKVALIDAVGLRNLRLDL 63				
Qy	105 LLGLENRNYTCVEVINGDCRQLAQYLRDKWMSNFELLICSKPRSKLPMGFGGKALEWLW 164				
Db	64 LLGLENRVTYNAMEFEGECQDIAQJATTPANEAVLVTDPITAIRDAVRTGILIECD 224				
Qy	165 DALKTRPEGSDFIIIDCPAGIDAGFTATPANEAVLVTDPITAIRDAVRTGILIECD				

Db	122	DSTRLR--NYNFILIDPAGIVDGFVNAAVAPAEAVVUTTPPEITSIRDADRVAGLLEAS	178	Db	192	DMIQKNDMMSSVRDVQEMLGIPLLGAPEUDSVLISTNKGEFLVNLKKLTSGIAFENAR	251
Qy	225	GIRDIKTYNRYRTDMIGEDMMSVLDYQEMLGISLIGYIPESEVIRSTNRGFPVLNK	284	Qy	299	RLV-BEDSMRKYMYEEPKRKFF---SFPGG	326
Db	179	GIREVKYLNVNRPEDMOTKNDMMSSVRDVQEMLGIPLLGAPEUDSVLISTNKGEFLVNLNK	238	Db	252	RLIGQD---VFIDLTSPOKCMFOKLQEFFPLG	280
Qy	285	PPTLAGLAFEQAWRLVQDSSMKAVMVEEPKRG	319				
Db	239	KLTLGSGPENAAARRV--GREYLYNLETGNG	270				
RESULT 2							
ID	MIND_CHLVU	STANDARD;	PRT;	282 AA.			
AC	P56346;						
DT	15-JUL-1998	(Rel. 36, Created)					
DT	15-JUL-1998	(Rel. 36, Last sequence update)					
DT	20-AUG-2001	(Rel. 40, Last annotation update)					
DE	PUTATIVE SEPTUM SITE-DETERMINING PROTEIN MIND.						
GN	MIND.						
OS	Guillardia theta (Cryptomonas phi).						
OG	Chloroplast.						
OC	Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales;						
CC	Chlorellaceae; Chlorella.						
OX	NCBI_TaxID=3077;						
[1]	SEQUENCE FROM N.A.						
RP	SEQUENCE STRAIN=N.A. STRAIN=C-27 / TAMIYA;						
RX	MEDLINE=97303241; PubMed=9159184;						
RA	Wakasugi T., Kapoor M., Sugita M., Ito M., Ito S.,						
RA	Tsudzuki T., Nagai T., Kapoor M., Sugita M., Ito M., Ito S.,						
RA	Inamura A., Nakashima K., Tsudzuki T., Suzuki Y., Hamada A., Ohta T.,						
RP	"Complete nucleotide sequence of the chloroplast genome from the green alga Chlorella vulgaris: the existence of genes possibly involved in chloroplast division"; Proc. Natl. Acad. Sci. U.S.A. 94:5967-5972(1997).						
RT	-!- FUNCTION: ATPase REQUIRED FOR THE CORRECT PLACEMENT OF THE DIVISION SITE (BY SIMILARITY).						
CC	-!- SIMILARITY: BELONGS TO THE PARA FAMILY. MIND SUBFAMILY.						
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CC	CC DR EMBL AF041468; AAC35621.1; -						
CC	CC DR InterPro; IPR000707; Para.						
CC	CC DR Pfam; PF00991; Para; 1.						
CC	CC KW Cell division; septation; ATP-binding; Chloroplast.						
CC	CC FT NP_BIND_10 17 ATP (POTENTIAL).						
CC	CC SQ SEQUENCE 29455 MW; BC363E954E689EA2 CRC64;						
CC	CC DR EMBL; AE001684; BA57951.1; -						
CC	CC DR InterPro; IPR000707; Para.						
CC	CC DR Pfam; PF00991; Para; 1.						
CC	CC KW Cell division; Septation; ATP-binding; Chloroplast.						
FT	NP_BIND_24 31013 MW; 94010DD45AE4AEC7 CRC64;						
SQ	SEQUENCE 28 AA:						
Query Match 42.0%							
DR	DR Best Local Similarity 55.9%, Pred. No. 5.1e-49;						
DR	DR Matches 146; Conservative 44; Mismatches 62; Indels 9; Gaps 3;						
DR	DR 59 RIVVITSGGGVKTNTANVGISLARYGFSVATADIGLRLMDLGLLENVNVTCE 11.8						
DR	DR 17 RVVITSGGGVKTNTANLGMSIARGYRALIDIGLRLMDLGLLENVNVTAM 7.6						
DR	DR 119 VINGCRUDQALVDRKWSNFELLICSKPRSKLPMGEGKALEWLVDLADTRGPSPDFI 17.8						
DR	DR 77 IVEGQRDQLARDKWNLLAISRNQK-YNTRKNNMLNIDSVK--ELGFDFV 13.1						
DR	DR 179 IIDCPAGIDAGEFTAITPANEAVLVTDPITALRDADRTVGLLECDGIRDIMVNVT 23.8						
Qy	59 RIVVITSGGGVKTNTANVGISLARYGFSVATADIGLRLMDLGLLENVNVTCE 11.8						
Qy	17 RVVITSGGGVKTNTANLGMSIARGYRALIDIGLRLMDLGLLENVNVTAM 7.6						
Qy	119 VINGCRUDQALVDRKWSNFELLICSKPRSKLPMGEGKALEWLVDLADTRGPSPDFI 17.8						
Qy	77 IVEGQRDQLARDKWNLLAISRNQK-YNTRKNNMLNIDSVK--ELGFDFV 13.1						
Qy	179 IIDCPAGIDAGEFTAITPANEAVLVTDPITALRDADRTVGLLECDGIRDIMVNVT 23.8						
Qy	132 IIDCPAGIDAGEFTAITPANEAVLVTDPITALRDADRTVGLLECDGIRDIMVNVT 23.8						
Qy	239 DMIGEDMMSSVRDVQEMLGIPLLGAPEUDSVLISTNKGEFLVNLKKLTSGIAFENAR						
Db	237 RL--DGQETEFLDLQSYSRG 254						

Query Match	31.6%	Score 523; DB 1; Length 268;	DR EMBL; AE000551; AAD07400.1; -.
Best Local Similarity	41.1%	Pred. NO. 3.4e-35;	DR TIGR; HP0331; -.
Matches	111;	Conservative	DR Interpro; IPR000392; Nitrogenase.II.
Matches	111;	68; Mismatches 77;	DR Interpro; IPR000392; Para.
Oy	181	DCAAGTAACTATTAATLGRKRVCLDGRNLVYMLGLENTRIVDVY 64	DR Pfam; PF00901; Para; 1.
Db	121	NGCRLDQALVVRKWSNELLCTSKPRSKLPLMGCGKAELWVDAKLPDPEGSDFPILL 190	DR Pfam; PF00901; Para; 1.
Db	65	EGRKCKHQZALKYKDRFDDL LYLHFAAQASDQTKAYAPEGIKNMQLKQ ---EFDYVII 119	RW cell division; separation; ATP-binding; Membrane; complete proteome.
Oy	180	LMNKGDITMDIDEVOHLSIDLQITAVSNHGEPTAMD -PKRASIAVNIARR 238	FT NP BIND 10 17 ATP (POTENTIAL).
Db	120	DCAFAGTCATTAIDANEAVLVWPDITALRDADRTGILC -DGARDIKMVKNRVRTD 239	SO SEQUENCE 268 AA; 29294 MW; 9E14766E8D10476 CRC6A;
Db	120	DCAFAGTCATTAIDANEAVLVWPDITALRDADRTGILC -DGARDIKMVKNRVRTD 239	Query Match 30.6%; Score 506.5; DB 1; Length 268;
Qy	240	MIGKEDMMSYLVDQEMLGLSLGVIPEDSEVIRSTNRGFLYLNKPPLAGLAFEQAANK 299	Best Local Similarity 40.1%; Pred. NO. 7.4e-34;
Db	180	LMMKGDITMDIDEVOHLSIDLQITAVSNHGEPTAMD -PKRASIAVNIARR 238	Mismatches 65; Conservative 65; Gaps 5;
Qy	300	LVEDDSMKAIVMVEEPKKRGFF ---SFPG 325	Matches 110; Cell division; separation; ATP-binding; Membrane.
Db	239	IL -GE SVPLQVLEEQNK -GMMAKIKSFFG 265	Qy 60 INGDCLRDQALYRDKRWSNELLCTSKPRSKLPLMGFGGGKALEWVDAKLPDPEGSDFPILL 179
RESULT	6	MIND_HELPY	Qy 64 MERNCNSQALTDKTRNLSPLAASQRKNDLKEKVAI --LILARL ---ADFDYL 117
ID	MIND_HELPY	STANDARD;	Db 64 MERNCNSQALTDKTRNLSPLAASQRKNDLKEKVAI --LILARL ---ADFDYL 117
AC	O25098;	PRT:	Db 118 LDSPAGIESGEEHALHADMALYVVTPEYSSURSDVYGLDASNRAKGMEVHKHLI 177
DT	20-AUG-2001 (Rel. 40, Created)		Qy 180 IDC PAC ID AGFITA ITPANEAVLWTTDITALRDADRTGILC -DGARDIK ---MI 232
DT	20-AUG-2001 (Rel. 40, Last sequence update)		Db 178 INRLKELVANGEMISIELEVKLICLPLIGITPDHHISATNKGEPVI - RTDCBSAKA 235
DE	SEQUENCE SITE-DETERMINING PROTEIN MIND (CELL DIVISION INHIBITOR MIND).		Qy 293 FEQAAMRVLVEODSMKAVMVEEPKKRGFFSFSGG 326
GN	MIND OR HP0331.		Db 236 YQTRTRIGEE ---VEVYEFRAKRGFFSALKG 265
OS	Helicobacter pylori (Campylobacter pylori).		RESULT 7
OC	Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;		ID MIND_HELPY STANDARD; PRT; 268 AA.
OC	Helicobacter		AC O25098;
OX	NCBI_TaxID=210;		DT 20-AUG-2001 (Rel. 40, Created)
RN	[1]		DT 20-AUG-2001 (Rel. 40, Last sequence update)
RP	SEQUENCE FROM N.A.		DE SEPTUM SITE-DETERMINING PROTEIN MIND (CELL DIVISION INHIBITOR MIND).
RC	STRAIN=26695 / ARCC 700392;		GN MIND OR JHP0314;
RX	MEDLINE=97394467; Pubmed=9252185;		RA Helicobacter pylori J99 (Campylobacter pylori J99).
RA	TOMO J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.C.,		OS Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
RA	Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,		OC Helicobacter.
RA	Nelson K., Quackenbush J., Zhou L., Kirkinis E.F., Peterson S.,		OC
RA	Loftus B., Richardson D., Dodson R., Khalak H.G., Glotzak A.,		ON Helicobacter.
RA	McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,		OC
RA	Berg D.E., Gooley J.D., Utterback T.R., Peterson J.D., Kelley J.M.,		ON
RA	Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E.,		RN [1]
RA	Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,		RP SEQUENCE FROM N.A.
RA	Venter J.C.;		RX MEDLINE=99120557; PubMed=9923687;
RT	"The complete genome sequence of the gastric pathogen Helicobacter		RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
RT	pylori."		RA Smith D.R., Noonan B., Guild B.C., de Jonge B.L., Carmel G.,
RL	CC -!- FUNCTION: ATPase required for the correct placement of the		RA Tumbino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
CC	division site cell division inhibitors Minc and Mind act in		RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
CC	concert to form an inhibitor capable of blocking formation of the		RA Trust T.J.,
CC	polar z ring septums. rapidly oscillates between the poles of the		RT "Genomic sequence comparison of two unrelated isolates of the human
CC	cell to destabilize FtsZ filaments that have formed before they		RT gastric pathogen Helicobacter pylori.".
CC	mature into polar z rings (by similarity).		RL Nature 397:176-180 (1999).
CC	CC -!- DIVISION SITE CELL DIVISION INHIBITORS MINC AND MIND ACT IN CONCERT TO FORM AN INHIBITOR CAPABLE OF BLOCKING FORMATION OF THE POLAR Z RING SEPTUMS. RAPIDLY OSCILLATES BETWEEN THE POLES OF THE CELL TO DESTABILIZE FTSZ FILAMENT THAT HAVE FORMED BEFORE THEY		CC FUNCTION: ATPase required for the correct placement of the
CC	CC -!- SUBUNIT: interacts with Minc and FtsZ (by similarity).		CC DIVISION SITE CELL DIVISION INHIBITORS MINC AND MIND ACT IN CONCERT TO FORM AN INHIBITOR CAPABLE OF BLOCKING FORMATION OF THE POLAR Z RING SEPTUMS. RAPIDLY OSCILLATES BETWEEN THE POLES OF THE
CC	CC -!- SUBCELLULAR LOCATION: membrane-associated (by similarity).		CC MATURE INTO POLAR Z RINGS (BY SIMILARITY).
CC	CC -!- SIMILARITY: belongs to the para family. mind subfamily.		CC SUBUNIT: interacts with Minc and FtsZ (by similarity).
CC	CC -!- This SWISS-PROT entry is copyright. It is produced through a collaboration		CC -!- SIMILARITY: BELONGS TO THE PARA FAMILY. MIND SUBFAMILY.
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CC STRAIN=K12;
 RC PubMed=8905232;
 RX MEDLINE=97061202;
 RA Oshima T., Aba H., Baba T., Fujita K., Hayashi K., Honjo A.,
 RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
 RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
 RA Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
 RA Sanpei G., Seki Y., Tagami H., Takemoto K., Wada C.,
 RA Yano M., Horuchi T.;
 RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome
 RT corresponding to the 12.7-28.0 min region on the linkage map.";
 RL DNA Res. 3:17-155(1996).
 RN [4]
 SQ RP SEQUENCE OF 1-12.
 RC STRAIN=K12 / EMG2;
 RX PubMed=9298646;
 RA Link A.J., Robison K., Church G.M.;
 RT "Comparing predicted and observed properties of proteins encoded
 RT in the genome of Escherichia coli K-12.";
 RL Electrophoresis 18:1259-1313(1997).
 RN [5]
 RP FUNCTION AND MUTAGENESIS.
 RX MEDLINE=97443975; PubMed=9298646;
 RA Link A.J., Robison K., Church G.M.;
 DR Boer P.A., Crossley R.E., Hand A.R., Rothfield L.I.;
 RT "The Mind protein is a membrane ATPase required for the correct
 RT placement of the Escherichia coli division site.";
 RL Electrophoresis 18:1259-1313(1997).
 RN [6]
 RP CHARACTERIZATION.
 RX MEDLINE=9209557; PubMed=10220403;
 RA Raskin D.M., de Boer P.A.;
 RT "Rapid pole-to-pole oscillation of a protein required for directing
 RT division to the middle of Escherichia coli";
 RL Proc. Natl. Acad. Sci. U.S.A. 96:4971-4976(1999).
 CC [-] FUNCTION: ATPase REQUIRED FOR THE CORRECT PLACEMENT OF THE
 CC DIVISION SITE. CELL DIVISION INHIBITOR MIND ACT IN
 CC CONCERT TO FORM AN INHIBITOR CAPABLE OF BLOCKING FORMATION OF THE
 CC POLAR Z RING SEPTUMS. RAPIDLY OSCILLATES BETWEEN THE POLES OF THE
 CC CELL TO DESTABILIZE FTSZ FILAMENTS THAT HAVE FORMED BEFORE THEY
 CC MATURE INTO POLAR Z RINGS.
 CC [-] SUBUNIT: INTERACTS WITH MIND AND FTSZ.
 CC [-] SIMILARITY: BELONGS TO THE PARA FAMILY. MIND SUBFAMILY.
 CC -----

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Qy 60 IVVITSGGGVGKTTTANGLSLARYFSVVAIDADGLURNDLGLLENRNVNTCEV 119
 Db 4 VVTISGGGGVGKSTTANLAIGLAESGKKVVAVIDDGLRNLDMTLGLENRIVDVVD 63
 Matches 109; Best Local Similarity 39.8%; Score 500.5; Length 268;
 保守性 65; Pred. No. 2.2e-33; Indels 19; Gaps 5;
 Mismatches 81;

Qy 120 INGCDRLDQALVDRKWSNPNFLCLISKPRSKPLMGFFGKALEWLYDALKTREPGSPDFII 179
 Db 64 MEKNCLNSQALITDKTKTNLSFLAASQSKDNILKEKVAI-LINALR---ADEFYIL 117
 Qy 180 IDCAGIDAGFTAITPANEAVIWTTPDITALRDADVTLGECGIR-----DIKMI 232
 Db 118 IDSPAGIESGEHATLHDAMLVVTPVSSLRSDRVIGIDAKSNRAKSGEYVHKHLI 177
 Qy 233 VNRVRTDMIKGEDMSVLDQVMSLIGLISLIGVPEVSEVISITNRGPVLINKPPILAGLA 292
 Db 178 INRLKPELVANGEMSIIEVKILCPLIGIIPEDHHIISATNKGEVPI--RTDCESAKA 235
 Qy 293 FEAQAARLVEQDSMKAIVVEEPKRGFFSFFGG 326
 Db 236 YQTRTRILGEE---VEYEFKAKGFFSALKG 265

RESULT 8
 MIND_ECOLI STANDARD; PRT; 269 AA.
 ID MIND_ECOLI
 AC P18197;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE SEPTUM SITE-DETERMINING PROTEIN MIND (CELL DIVISION INHIBITOR MIND)
 GN MIND OR B1175.
 OC Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision: Enterobacteriaceae;
 OC Escherichia.
 RN NCBI_TAXID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89136010; PubMed=2645057;
 RA de Boer P.A.J., Crossley R.E., Rothfield L.I.;
 RT "A division inhibitor and a topological specificity factor coded for
 by the minicell locus determine proper placement of the division
 septum in E. coli.";
 RL Cell 56:641-649(1989).
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 RX MEDLINE=9746617; PubMed=9278503;
 RA Blattner F.R., Plunett G., III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rose C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:145-147(1997).
 RN [3]
 RP SEQUENCE FROM N.A.

Query Match 29.0%; Score 479; DB 1; Length 269;
 Best Local Similarity 39.9%; Pred. No. 1.2e-31;
 Matches 113; Conservative 58; Mismatches 82; Indels 30; Gaps 8;

QY	59	RIVVITSGGGVGGKTTTANVGLSLARYGSVVAIDADIGRLNLDLGLLENVRNYTCVE	118	SQ	SEQUENCE	271	AA:	29483	MW:	EC76D3F15D64A4CA	CRC64;	
Db	2	RIVVITSGGGVGGKTTTANVGLSLARYGSVVAIDADIGRLNLDLGLLENVRNYTCVE	61	Query Match	28.7%	Score	475.5;	DB	1;	Length	271;	
				Best Local Similarity	40.9%	Pred.	No.	2.4e-31;				
				Matches	105;	Conservative	47;	Mismatches	68;	Indels	37;	
											5;	
QY	119	VINGDCRDLQALVDRDKRWSMFEILCISPKRSKLPMGFGCKAKALEIVDAALKTRPGCSDDFI	178	QY	60	IIVVITSGGGVGGKTTTANVGLSLARYGSVVAIDADIGRLNLDLGLLENVRNYTCVE	119	Db	4	VIVVITSGGGVGGKTTTANVGLSLARYGSVVAIDADIGRLNLDLGLLENVRNYTCVE	63	
Db	62	VQGDATUNQLQALDKRTRNLQIIFASQTRKDALTREGVAK--VLDUDKAM--DFFEF	116	QY	120	INGDCRDLQALVDRDKRWSMFEILCISPKRSKLPMGFGCKAKALEIVDAALKTRPGCS	--	175	Db	4	VIVVITSGGGVGGKTTTANVGLSLARYGSVVAIDADIGRLNLDLGLLENVRNYTCVE	63
QY	179	IIDPGAGIDAGPFTAITPAANEAVLVTPDTIALDADRTVGLLEC-	-DGFDIK--	QY	120	INGDCRDLQALVDRDKRWSMFEILCISPKRSKLPMGFGCKAKALEIVDAALKTRPGCS	--	175	Db	4	VIVVITSGGGVGGKTTTANVGLSLARYGSVVAIDADIGRLNLDLGLLENVRNYTCVE	63
Db	117	VCDSPLAGETGAALMAYFADEALLTNPVSSVSDRDLGILASKSRAENGEEPIKEH	176	QY	124	VNGKVSPQEALVKHMKLNLYL--PASO-----	--	103	Db	64	VNGKVSPQEALVKHMKLNLYL--PASO-----	--
QY	231	MIYNVRVTDMIKGEDMMSYLDQEMRLGSLSLGVLIPEDSEYITRSTNRGEFLYKPTLAG	290	QY	176	--DFTIDINOCAGIDAGFTITATPANEAVLVTPDTIALDADRTVGLLEC	DG	225	Db	64	VNGKVSPQEALVKHMKLNLYL--PASO-----	--
Db	177	LLETRVNPORVSQDSMGSNDVEILDLRKIVGVPEDQSYLRAASNQGEVILDINAD-AG	235	QY	176	--DFTIDINOCAGIDAGFTITATPANEAVLVTPDTIALDADRTVGLLEC	DG	225	Db	104	AIVKELIPHDFYIIDSPLAGIERGFNAVADAERVLVTTPLDAISDAVRVCLENFG	163
QY	291	LAFQQAANLVEQDSMKAWVVEEP-----KKGFFFS-FFGG	326	QY	226	IRD--IKMVYNVRVTDMIKGEDMMSYLDQEMRLGSLSLGVLIPEDSEYITRSTNRGEFLYKPTLAG	290	Db	164	FSDERINVITNRPDPIMVRKGEMLTDDIKRTLSLSELIAVIPDSEDIVASNTG	IPVSLN	
Db	236	KAY-----ADVERLGEERPFERIEERKGFLKRFFGG	269	QY	284	KPPTLAGLAFQDAAWRL	300	Db	224	GNSRIS-KNFENLARKI	239	
<hr/>												
RESULT 9												
MIND_THEME	9	MINd_THEME	STANDARD:	PRT:	271	AA:						
AC	Q9XK33;	ID	MIND_THEME	STANDARD:								
DT	20-AUG-2001	(Rel.	40;	Created)								
DT	20-AUG-2001	(Rel.	40;	Last sequence update)								
DT	20-AUG-2001	(Rel.	40;	Last annotation update)								
DE	SEQUENCE SITE-DETERMINING PROTEIN MIND	(CELL DIVISION INHIBITOR MIND)										
GN	MIND OR TM1870											
OS	Bacteria											
OC	Thermotoga											
OX	Thermotoga maritima											
RN	NCB TaxID=2336;											
RN	SEQUENCE FROM N.A.											
RC	STRAIN=M588 / DSM 3109;											
RC	MEDLINE=99287116; PubMed=10360571;											
RA	Nelson K.E., Clayton R.A., Gill S.R., Gwynn M.L., Dodson R.J.,											
RA	Hait D.H., Hickey E.K., Peterback J.D., Nelson W.C., Ketchum K.A.,											
RA	McDonald L., Utterback T.R., Malek J.A., Linher R.B., Garrett M.M.,											
RA	Stewart A.M., Cottam M.D., Pratt M.S., Phillips C.A., Richardson D.,											
RA	Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,											
RA	Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.,											
RT	"Evidence for lateral gene transfer between Archaea and Bacteria from genome sequence of the thermotoga maritima."											
RL	Nature 399:321-329(1999).											
CC	- FUNCTION: ATPase required for the correct placement of the											
CC	DIIVISION SITE. CELL DIVISION INHIBITORS MIND AND MIND ACT IN CONCERT TO FORM AN INHIBITOR CAPABLE OF BLOCKING FORMATION OF THE POLAR Z RING SEPTUMS. RAPIDLY OSCILLATES BETWEEN THE POLES OF THE CELL TO DESTABILIZE FTZ FILMENTS THAT HAVE FORMED BEFORE THEY MATURE INTO POLAR Z RINGS (BY SIMILARITY).											
CC	- SUBUNIT: INTERACTS WITH MIND AND FTsz (BY SIMILARITY).											
CC	- SUBCELLULAR LOCATION: MEMBRANE ASSOCIATED (BY SIMILARITY).											
CC	- SIMILARITY: BELONGS TO THE PARA FAMILY. MIND SUBFAMILY.											
CC	- - - - -											
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).											
CC	EMBL: AP001024; AD36932; -											
DR	TIGI; TM1870; -											
DR	InterPro: IPR000392; NitrogenaseII.											
DR	InterPro: IPR000707; Para.											
DR	Pfam: PF00142; recf_NIIF; 1.											
DR	Pfam: PF00991; Para; 1.											
KW	Cell division; Septation; ATP-binding Membrane; Complete proteome.											
FT	INT_MET 0 0 0 BY SIMILARITY.											
FT	NP_BIND 9 16 ATP (POTENTIAL).											

RESULTS

AC P57411; DT 20-AUG-2001 (Rel. 40; Created) DT 20-AUG-2001 (Rel. 40; Last sequence update) DT 20-AUG-2001 (Rel. 40; Last annotation update) DE SEPTUM SITE-DETERMINING PROTEIN MIND (CELL DIVISION INHIBITOR MIND). OS Buchnera aphidicola (subsp. *Acyrthosiphon pisum*) (SYMBIOTIC bacterium) OS symbiotic bacterium) OC NCBI_TaxID=118099; RT Buchnera sp. APs;" RT Buchnera sp. APs;" RL SEQUENCE FROM N.A. [1] FUNCTION: ATPase required for the correct placement of the division site. Cell division inhibitors MIND and MIND ACT IN CONCERT TO FORM AN INHIBITOR CAPABLE OF BLOCKING FORMATION OF THE POLAR 2 RING SEPTUMS. RAPIDLY OSCILLATES BETWEEN THE POLES OF THE CELL TO DESTABILIZE FTZ FILMENTS THAT HAVE FORMED BEFORE THEY MATURE INTO POLAR Z RINGS (BY SIMILARITY). CC -1- SUBUNIT: INTERACTS WITH MIND AND FTsz (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: MEMBRANE ASSOCIATED (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE PARA FAMILY. MIND SUBFAMILY.

CC - - - - -

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EMBL: AP001110; BAB12034; 1; DR InterPro; IPR000707; Para. DR Pfam; PF00991; Para; 1. KW Cell division; Septation; ATP-binding Membrane; Complete proteome. FT INT_MET 0 0 0 BY SIMILARITY. NP_BIND 9 16 ATP (POTENTIAL).

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OM protein - protein search, using sw model

Run on: February 11, 2002, 13:31:13 ; Search time 16.09 Seconds
(without alignments)
1543.375 Million cell updates/sec

Title: US-09-553-431-2
Perfect score: 1654
Sequence: 1 MASLRLFSTNHQSLLLSSL.....KAVMVEBBPKKRGGFFSFPGG 326

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68:
1: pir1:
2: pir2:
3: pir3:
4: pir4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7.92	47.9	282	2 T07303	cell division inhi
2	64.3	38.9	266	2 S16970	hypothetical prote
3	57.5	34.7	276	2 D15478	septum site-determ
4	536.5	32.4	264	2 C84028	septum site-determ
5	523	31.6	268	1 G15239	cell division inhi
6	516	31.2	262	2 F70375	cell division inhi
7	514.5	31.1	269	2 C82695	septum site-determ
8	506.5	30.6	268	2 C64561	cell division inhi
9	500.5	30.3	268	2 B71945	cell division inhi
10	480.5	29.1	271	2 F83239	cell division inhi
11	479	29.0	270	1 CCBCID	hypothetical prote
12	479	29.0	270	2 F05695	septum site-determ
13	475.5	28.7	271	2 A72200	septum site-determ
14	468	28.3	276	2 C81136	septum site-determ
15	460	27.8	270	2 B84968	septum site-determ
16	449.5	27.2	271	2 C81230	septum site-determ
17	366	22.1	260	2 F75175	cell division inhi
18	344.5	20.8	259	2 B69113	probable cell divi
19	341.5	20.6	245	2 C71105	cell division inhi
20	335	20.3	263	2 H9336	cell division inhi
21	327.5	19.8	245	2 A75056	cell division inhi
22	300	18.1	264	1 C64368	hypothetical prote
23	266	16.1	252	2 F71191	cell division inhi
24	262.5	15.9	305	2 A84363	probable cell divi
25	254	15.4	217	2 H71038	flagellar synthesis
26	249	15.1	280	2 B84463	cell division inhi
27	247.5	15.0	251	2 H7150	hypothetical prote
28	246.5	14.9	288	2 D82954	cell division inhi
29	243.5	14.7	323	2 B84251	A;Variety: pcc 6803

ALIGNMENTS

RESULT 1
T07303
cell division inhibitor - Chlorella vulgaris chloroplast
C;Species: chloroplast Chlorella vulgaris
C;Date: 14-May-1999 #sequence_change 21-Jul-2000
C;Accession: T07303
R;Kawasugi, T.; Nagai, T.; Kapoor, M.; Sugita, M.; Ito, S.; Tsudzuki, J.; Na
Proc. Natl. Acad. Sci. U.S.A. 94, 5967-5972, 1997
A;Title: Complete nucleotide sequence of the chloroplast genome from the green alga C
A;Reference number: 215985; MUID:9/303241
A;Accession: T07303
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-282 <WAK>
A;Cross-references : EMBL:AB001684; PIDN:BAAS7951.1; PID:g2224467
C;Genetics:
A;Gene: mind
A;Genome: chloroplast
C;Superfamily: cell division inhibitor mindD
C;Keywords: chloroplast

Query Match 47.9%; Score 792; DB 2; Length 282;
Best Local Similarity 60.4%; Pred. No. 4.6e-55; Mismatches 55; Indels 14; Gaps 5;

Matches 165; Conservative 39; Mismatches 55; Indels 14; Gaps 5;

Qy 59 RIVITSGKGGVKTTTANVGLSLARNGFESVVAIDADIGLRLNDLGLLENRYNTCYE 118
Db 17 RVIVITSGKGGVKTTTANLGMSLARLGYRVALIDADIGLRLNDLGLLENRYLYTAMD 76

Qy 119 VINGDCRLLDQALYEDKRWNSFELICISPKRSKLPMGFGKALEWIVDAIKTRPESPDFI 178
Db 77 IVEGSQCRLLDQALYEDKRWNLALLAISKRKQ - YNVTRKMNQLIDSVK - - ELGFQFVY 131

Qy 179 LIDCPAGIDAGEFTAITPANEAVLVTPDTIALRDADRYTGLFCDCGIRDIKMTVNRYT 238
Db 132 LIDCPAGIDAGEFTAITPDTIALRDADRYTGLFCDCGIRDIKMTVNRYTINVKLIVNVRVP 191

Qy 239 DMIGKEDAMSVLDQEMGLSLLGIVPDESEVIRSTNRGEPLVLNKPPLLAGLFLAEQQAW 298
Db 192 DMIQKNDMSVDRQEMGLGIPLGAIPDTSVILSTNGKEPLVLNKKLTSGTAFENAA 251

Qy 299 RLV-EQDSMKAVMVEEPKKGFF---SFFGG 326
Db 252 RLIGKQD---YFIDLTSFQKGMFQKLQEFLG 280

RESULT 2
S76970 hypothetical protein - Synechocystis sp. (strain PCC 6803)
C;Species: Synechocystis sp.
A;Variety: pcc 6803

C; Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
 C; Accession: S76970
 R; Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
 o, R.; Okumura, S.; Shimpou, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
 DNA Res. 3, 109-136, 1996.
 A; Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
 s.
 A; Reference number: S74322; MUID:97061201
 A; Accession: S76970
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1 266 (KAN)
 A; Cross-references: EMBL:D64005; GB:AB001339; NID:91001779; PIDN:BAAL0662_1; PID:9100178
 A; Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
 C; Superfamily: Cell division inhibitor mind

Query Match 38.9%; Score 643; DB 2; Length 266;
 Best Local Similarity 52.8%; Pred. No. 3.6e-44;
 Matches 130; Conservative 51; Indels 6; Gaps 2;

RESULT 4
 C84028 septum site-determining protein mind [imported] - Bacillus halodurans (strain C-125)
 C; Species: Bacillus halodurans
 C; Date: 01-Dec-2000 #text_change 08-Dec-2000
 C; Accession: C84028
 R; Nakano, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; i H
 Nucleic Acids Res. 28, 4317-4331, 2000
 A; Title: Complete genome sequence of the alkaliophilic bacterium Bacillus halodurans a
 A; Reference number: A83650; MUID:20263314
 A; Accession: C84028
 A; Status: preliminary
 A; Molecular type: DNA
 A; Residues: 1 264 <STOP>
 A; Cross-references: GB:AP001517; GB:BA000004; PIDN:BA06746_1; CSPDB:G
 A; Experimental source: strain C-125
 C; Genetics:
 A; Gene: mind
 C; Superfamily: cell division inhibitor mind

Query Match 32.4%; Score 536.5; DB 2; Length 264;
 Best Local Similarity 41.1%; Pred. No. 1.2e-35;
 Matches 109; Conservative 66; Mismatches 83; Indels 7; Gaps 3;

RESULT 5
 C84028 septum site-determining protein mind [imported] - Bacillus halodurans (strain C-125)
 C; Accession: C84028
 R; Nakano, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; i H
 Nucleic Acids Res. 28, 4317-4331, 2000
 A; Title: Complete genome sequence of the alkaliophilic bacterium Bacillus halodurans a
 A; Reference number: A83650; MUID:20263314
 A; Accession: C84028
 A; Status: preliminary
 A; Molecular type: DNA
 A; Residues: 1 264 <STOP>
 A; Cross-references: GB:AP001517; GB:BA000004; PIDN:BA06746_1; CSPDB:G
 A; Experimental source: strain C-125
 C; Genetics:
 A; Gene: mind
 C; Superfamily: cell division inhibitor mind

Query Match 32.4%; Score 536.5; DB 2; Length 264;
 Best Local Similarity 41.1%; Pred. No. 1.2e-35;
 Matches 109; Conservative 66; Mismatches 83; Indels 7; Gaps 3;

Query Match 61 VVITSGKGVGTTTANVGLSLARYGFSVVAIDALGLRNLDLIGLENRYTCYEVYI 120
 C; Species: Deinococcus radiodurans
 C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
 C; Accession: D75748
 R; White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
 M.; Shien, M.; Vanathavan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma,
 S.; Smith, H.O.; Ventler, J.C.; Fraser, C.M.
 Science 286, 1571-1577, 1999
 A; Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
 A; Reference number: A75250; MUID:20036896
 A; Accession: D75748
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-276 <WHR>
 A; Cross-references: GB:AE001931; GB:AE000513; NID:96458461; PIDN:AAF10331_1; PID:9645846
 A; Experimental source: strain R1
 A; Genetics:
 A; Gene: DR0752
 A; Map position: 1
 C; Superfamily: cell division inhibitor mind

RESULT 5
 G45239 cell division inhibitor mind [validated] - Bacillus subtilis
 N; Alternative names: septum placement determinant mind
 C; Species: Bacillus subtilis
 C; Date: 10-Jun-1993 #sequence_revision 04-Oct-1996 #text_change 19-Jan-2001
 C; Accession: S31205; G45239; F45240; A696550; S27521; S28866
 R; Lee, S.-i; Price, C.W.
 Mol. Microbiol. 7, 601-610, 1993

Query Match 34.7%; Score 573.5; DB 2; Length 276;
 Best Local Similarity 44.3%; Pred. No. 1.4e-38;
 Matches 125; Conservative 52; Mismatches 72; Indels 33; Gaps 5;

Query Match 59 VVITSGKGVGTTTANVGLSLARYGFSVVAIDALGLRNLDLIGLENRYTCYEVYI 118
 C; Species: Deinococcus radiodurans
 C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
 C; Accession: D75748
 R; White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
 M.; Shien, M.; Vanathavan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma,
 S.; Smith, H.O.; Ventler, J.C.; Fraser, C.M.
 Science 286, 1571-1577, 1999
 A; Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
 A; Reference number: A75250; MUID:20036896
 A; Accession: D75748
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-276 <WHR>
 A; Cross-references: GB:AE001931; GB:AE000513; NID:96458461; PIDN:AAF10331_1; PID:9645846
 A; Experimental source: strain R1
 A; Genetics:
 A; Gene: DR0752
 A; Map position: 1
 C; Superfamily: cell division inhibitor mind

RESULT 5
 G45239 cell division inhibitor mind [validated] - Bacillus subtilis
 N; Alternative names: septum placement determinant mind
 C; Species: Bacillus subtilis
 C; Date: 10-Jun-1993 #sequence_revision 04-Oct-1996 #text_change 19-Jan-2001
 C; Accession: S31205; G45239; F45240; A696550; S27521; S28866
 R; Lee, S.-i; Price, C.W.
 Mol. Microbiol. 7, 601-610, 1993

A; Title: The minCD locus of *Bacillus subtilis* lacks the minE determinant that provides A; Reference number: S31204; MUID:33211302
A; Molecule type: DNA
A; Accession: S31205
A; Residues: 1-268 <LEV>
A; Cross-references: EMBL:215113; NID:949307; PIDN:CAA78818.1; PID:9580893
R; Levin, P.A.; Margolis, P.S.; Setlow, P.; Losick, R.; Sun, D.
J; Bacteriol. 174, 6717-6728, 1992
A; Title: Identification of *Bacillus subtilis* genes for septum placement and shape determinants A; Reference number: A45239; MUID:33015731
A; Status: not compared with conceptual translation
A; Molecule type: DNA
A; Residues: 1-268 <LEV>
A; Cross-references: GB:M96343; NID:9142852; PIDN:AAA22401.1; PID:9142859
A; Note: sequence extracted from NCBI backbone (NCBIP:116563)
R; Varley, A.W.; Stewart, G.C.
J; Bacteriol. 174, 6729-6742, 1992
A; Title: The divIVB region of the *Bacillus subtilis* chromosome encodes homologs of Escherichia coli minC and minD A; Reference number: A45240; MUID:93015731
A; Accession: F45240
A; Molecule type: DNA
A; Residues: 1-268 <VA>
A; Cross-references: EMBL:M95582; NID:9143211; PIDN:AAA22609.1; PID:g143216
A; Note: sequence extracted from NCBI backbone (NCBIP:116574)
R; Kunst, F.; Ogasawa, N.; Albertini, A.M.; Alion, G.; Azevedo, V.; Berten, C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho, A.; Ehrlich, S.D.; Emmerison, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.; Nature 390, 249-256, 1997
A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holzapfel, S.; Hosono, S.; Hull, M.F.; Koetter, P.; Koningsstein, G.; Krogh, S.; Kurata, M.; Kurita, K.; Lapidus, A.; Lardinois, Y.; M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, R.; Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Satoh, T.; Scanlon, A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowaka, A.; Seror, akuchi, M.; Tamakoshi, A.; Tanaka, T.; Terrostra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasuno, K.; Yoshida, K.; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A; Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*. A; Reference number: A69380; MUID:98044033
A; Accession: A69658
A; Molecule type: DNA
A; Residues: 1-268 <KUN>
A; Cross-references: GB:Z99118; GB:AL009126; NID:92635200; PIDN:CA14759.1; PID:92635264
A; Status: nucleic acid sequence not shown; translation not shown
A; Function: minD
A; Start codon: ATG
C; Description: mediates, together with minC, cell division site selection by specifically controlling the minC promoter A; Genetics:
F; 10-17/Region: nucleotide-binding motif A (P-loop)
F; 16/Binding site: ATP (Lys) #status predicted

Query Match 31.6%; Score 523; DB 1; Length 268;
Best Local Similarity 31.1%; Pred. No. 1.5e-34;
Matches 111; Conservative 68; Mismatches 77; Indels 14; Gaps 7;

QY 61 VVITSGKGKVKTTSANGTATAILGRVKCLWDIGRLNDVMLGLENRTIDLVVV 64
Db 5 IVITSGKGKVKTTSANGTATAILGRVKCLWDIGRLNDVMLGLENRTIDLVVV 64
QY 121 NGDCRLDOALVRDKRWSNFELLCISKPRSKLPMGFGKAKLEWLWALKTRPEGSPDFII 180
Db 65 EGRCRMHQALVKDRFDDLL-LYVKAQPSDKTAVAPEQKNNQELKQ ----EFDVVII 19
QY 181 DCPAGIDAGFITATPANEAVLVTTPDITALRADRVTLGLEC-DGIRDIKMIVNRVRTD 239
Db 120 DCAPAGIEQYKNAVGADRAIVVTPPEISAVRDRIGLEQUEENIEPRLVYNIRNH 179

RESULT 7
C82695 31.6%; Score 523; DB 1; Length 268;
C; Species: Xylella fastidiosa (strain 9a5c)
C; Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C; Accession: C82695
R; anonymous. The *Xylella fastidiosa* Consortium of the Organization for Nucleotide Seq Nature 40(6), 151-157, 2000
A; Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.
A; Reference number: A82515; MUID:20365717
A; Note: for a complete list of authors see reference number A59328 below
A; Accession: C82695

QY 298 WRLEQDSMKAYWEEEEKKR 318
Db 234 -----DTARRLMGESEIFLKR 248

RESULT 7
C82695 31.6%; Score 523; DB 1; Length 268;
C; Species: Xylella fastidiosa
C; Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C; Accession: C82695
R; anonymous. The *Xylella fastidiosa* Consortium of the Organization for Nucleotide Seq Nature 40(6), 151-157, 2000
A; Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-269 <SIM>
A; Cross-references: GB:AE003965; PIDN:AAF84130.1; GSPDB:GN

A;Experimental source: strain 945C	Query Match	30.6%	Score 506.5;	DB 2;	Length 268;	
R;Simpson, A.J.G.; Reinhach, F.C.; Arruda, P.; Abreu, F.A.; Aceñolá, M.; Alvarenga, R.; Britones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Carrasco, D.M.; Carrer, P.; Netto, E.; Docena, C.; El-Dorri, H.; Faccianci, A.P.; Ferreira, A.J.S.	Best Local Similarity	40.1%	Pred. No. 3.1e-33;			
Submitted to GenBank, June 2000	Matches	110;	Conservative	65;	Mismatches 80;	
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Praga, J.S.; França, S.C.; Franco, M.C.; Froehl, J.D.; Junqueira, M.L.; Kempfer, E.L.; Kurama, J.P.; Krieger, J.B.; Mariano, E.B.; Marins, E.; Martins, E.M.F.; Madeira, A.M.B.N.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; Nunes, L.R.; Oliveira, M.A.; Oliveira, R.C.; Palmeiro, D.A.; Rodrigues, V.; Rosa, R.G.; Santelli, R.Y.; Soawas, A.; Tsuchiya, M.H.; Valada, H.; van Siuys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; G;Contents: annotation	Indels	19;	Gaps	5;		
C;Genetics: XFL1321	Qy	60	IYVITSGKGGVKTATTANGLSLRSPRSKLPNGFGGKALEWLYDALTRPESPDFII 179	Db	4	VVTITSGKGGVKTATTANGLSLRSPRSKLPNGFGGKALEWLYDALTRPESPDFII 179
C;Superfamily: cell division inhibitor mind	Db	120	INGDCRLDQLYDKRWSNPFELLCSKPKRSKLPMGFGKKALEWLYDALTRPESPDFII 179	Qy	60	IVVITSGKGGVKTATTANGLSLRSPRSKLPNGFGGKALEWLYDALTRPESPDFII 179
C;Accession: AJ3126	Db	64	IBEBATLQKALIDKRFDNLYLAAQPRDKDALTKEC-VEVKVNELOA--BGP-DVTC 118	Qy	64	IBEBATLQKALIDKRFDNLYLAAQPRDKDALTKEC-VEVKVNELOA--BGP-DVTC 118
C;Function: an ATPase required for correct placement of cell division site	Db	180	IDCPAGIDAGFITAIPANEAVLYTPDITALDADRTVGLI-EDCGIR-----ADFDYL 117	Qy	180	IDCPAGIDAGFITAIPANEAVLYTPDITALDADRTVGLI-EDCGIR-----ADFDYL 117
C;Description: cell division inhibitor mind	Db	119	CDSPAGIEKGASALAMYDRAVYVNPPEVSVSDRIGLSDSKTKKAETGSSITRIL 178	Qy	119	CDSPAGIEKGASALAMYDRAVYVNPPEVSVSDRIGLSDSKTKKAETGSSITRIL 178
C;Keywords: ATP; cell division control; nucleotide binding; p-loop	Db	233	VNRVRTDMIKGEDMMSVLDVQEMLGSLSELGVDEDESEVTRSTRGFPVLNKPLLAGIA 292	Qy	233	VNRVRTDMIKGEDMMSVLDVQEMLGSLSELGVDEDESEVTRSTRGFPVLNKPLLAGIA 292
C;16/Binding site: ATP (Lys) #status predicted	Db	179	LTRYSPARVESGEMLSIADVEEVIGLKAIGVIESGVLDNLNSLAGLA 237	Qy	179	LTRYSPARVESGEMLSIADVEEVIGLKAIGVIESGVLDNLNSLAGLA 237
C;Accession: C64561	Qy	293	FEQAANRLLVEQD-SMKAVMVEEPKPKRGFFS-BFGG 326	Db	293	FEQAANRLLVEQD-SMKAVMVEEPKPKRGFFS-BFGG 326
C;Function: an ATPase required for correct placement of cell division site	Db	238	YEDAVGRILGEDHPMRFTVE--KKGFFSKLFGG 269	Qy	238	YEDAVGRILGEDHPMRFTVE--KKGFFSKLFGG 269
C;Description: cell division inhibitor mind	Db	293	FEQAANRLLVEQD-SMKAVMVEEPKPKRGFFS-BFGG 326	Qy	293	FEQAANRLLVEQD-SMKAVMVEEPKPKRGFFS-BFGG 326
C;Keywords: ATP; cell division control; nucleotide binding; p-loop	Db	236	YQRTRRLGEE---VEVVFKAKGFFSALKG 265	Qy	236	YQRTRRLGEE---VEVVFKAKGFFSALKG 265

RESULT 10
 F83239 cell division inhibitor Mind PA3244 [imported] - *Pseudomonas aeruginosa* (strain PA01)
 C;Species: *Pseudomonas aeruginosa*
 C;Accession: F83239
 C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Brandom, S.; Yuan, Y.; Boddy, L.I.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A;Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen
 A;Reference number: A82950; MUID:20437337
 A;Accession: F83239
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-271 <STOP>
 A;Cross references: GB:AE004747; GB:AE004091; NID:99949362; PIDN:AAG06632.1; GSPDB:GN001
 A;Experimental source: strain PA01
 C;Genetics:
 A;Gene: mind; PA3244
 C;Superfamily: cell division inhibitor mind

Query Match 29.1%; Score 480.5; DB 2; Length 271;
 Best Local Similarity 39.6%; Pred. No. 3.8e-31; Indels 35; Gaps 7;
 Matches 113; Conservative 54; Mismatches 83; Indels 35; Gaps 7;

Qy 59 RIVVITSGGGVCKTMTTANVGLSLARYGFSVVAIDADIGLRLNDLGLLENRNYTCVE 118
 Db 3 RIVVITSGGGVCKTMTTANVGLSLARYGFSVVAIDADIGLRLNDLGLLENRNYTCVE 118
 Qy 119 VINGDCRDLQALVRDKRNSNELLICPRSKLPMGFFGKALEWLYDAL---KTRP 172
 Db 63 VINGDCRDLQALVRDKRNSNELLICPRSKLPMGFFGKALEWLYDAL---KTRP 172
 Qy 179 IIDCPAGIDAGFITAATPANEAVLVTPDITALRDADRTVGLILE 230
 Db 119 VINGDCRDLQALVRDKRNSNELLICPRSKLPMGFFGKALEWLYDAL---KTRP 172
 Qy 231 MIVNRVRDTMIKGEDMMSVLDQEMILGSLLGVIPDESEVIRSTINRGFLVLNKPTLKG 290
 Db 178 LLITTRYNPGRVSQSDMLSMEDVLEILRKLVKGVPQEVLSRASQNQEPVILDINAD-AG 236
 Qy 291 LAFFQAAWRVLEODSMKKAVNEEPP---KRGFFS-FFGG 326
 Db 237 KAY -----ADTVRELGEERPFRTIEEKKGFLKLFQGG 270

RESULT 12
 F83695 hypothetical protein mind [imported] - *Escherichia coli* (strain O157:H7)
 C;Species: *Escherichia coli* (strain O157:H7)
 C;Accession: F83695
 C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
 R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayr, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potanousis, K.; Apoda
 Nature 409, 529-533, 2001
 A;Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.
 A;Reference number: A85480; MUID:21074935; PMID:11206551
 A;Accession: F83695
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-270 <STOP>
 A;Cross-references: GB:J03153; NID:9146865; PIDN:AAB59062.1; PID:9146867
 C;Sequence: Escherichia coli
 C;Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 19-Jan-2001
 C;Accession: B31877; D64663
 R;de Boer, P.A.J.; Crossley, R.E.; Rothfield, L.I.
 Cell 56, 641-649, 1989
 A;Title: A division inhibitor and a topological specificity factor coded for by the mini CCECD
 cell division inhibitor mind - *Escherichia coli*
 N;Alternate names: septum site-determining protein mind
 C;Species: *Escherichia coli*
 C;Accession: B31877
 R;de Boer, P.A.J.; Crossley, R.E.; Rothfield, L.I.
 Cell 56, 641-649, 1989
 A;Reference number: A31877; MUID:89136010
 A;Accession: B31877
 A;Molecule type: DNA
 A;Residues: 1-270 <DB>
 A;Cross-references: GB:J03153; NID:9146865; PIDN:AAB59062.1; PID:9146867
 R;Blattner, F.R.; Plunkett III, G.; Perna, N.T.; Burland, V.; Riley, M.; Cole, R.; Rose, D.J.; Mau, B.; Shao, Y.
 Science 277, 1453-1462, 1997
 A;Title: The complete genome sequence of *Escherichia coli* K-12.
 A;Reference number: A64720; MUID:9146617
 A;Accession: D64863
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-270 <BLAT>
 A;Cross-references: GB:AE000216; GB:U00096; NID:91787417; PIDN: AAC74259.1; PID:91787423;

A;Experimental source: strain K-12, substrate MG1655
 C;Genetics:
 A;Gene: mind
 A;Map position: 26 min
 C;Function:
 A;Description: a membrane ATPase required for correct placement of cell division site
 A;Note: minC and mind act in concert to form an inhibitor capable of blocking formation found between ftsZ and minD
 C;Superfamily: cell division inhibitor mind
 C;Keywords: ATP; cell division control; nucleotide binding; P-loop
 F;10-17/Region: nucleotide-binding motif A (P-loop)
 F;16/Binding site: ATP (lys) #status predicted
 F;16/Binding site: ATP (lys) #status predicted

Query Match 29.0%; Score 479; DB 1; Length 270;
 Best Local Similarity 39.9%; Pred. No. 5e-31; Indels 30; Gaps 8;
 Matches 113; Conservative 58; Mismatches 82; Indels 30; Gaps 8;

Qy 59 RIVVITSGGGVCKTMTTANVGLSLARYGFSVVAIDADIGLRLNDLGLLENRNYTCVE 118
 Db 3 RIVVITSGGGVCKTMTTANVGLSLARYGFSVVAIDADIGLRLNDLGLLENRNYTCVE 118
 Qy 119 VINGDCRDLQALVRDKRNSNELLICPRSKLPMGFFGKALEWLYDAL---KTRP 172
 Db 63 VINGDCRDLQALVRDKRNSNELLICPRSKLPMGFFGKALEWLYDAL---KTRP 172
 Qy 179 IIDCPAGIDAGFITAATPANEAVLVTPDITALRDADRTVGLILE 230
 Db 119 VINGDCRDLQALVRDKRNSNELLICPRSKLPMGFFGKALEWLYDAL---KTRP 172
 Qy 231 MIVNRVRDTMIKGEDMMSVLDQEMILGSLLGVIPDESEVIRSTINRGFLVLNKPTLKG 290
 Db 178 LLITTRYNPGRVSQSDMLSMEDVLEILRKLVKGVPQEVLSRASQNQEPVILDINAD-AG 236
 Qy 291 LAFFQAAWRVLEODSMKKAVNEEPP---KRGFFS-FFGG 326
 Db 237 KAY -----ADTVRELGEERPFRTIEEKKGFLKLFQGG 270

RESULT 13
 F83695 hypothetical protein mind [imported] - *Escherichia coli* (strain O157:H7)
 C;Species: *Escherichia coli* (strain O157:H7)
 C;Accession: F83695
 C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
 R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayr, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potanousis, K.; Apoda
 Nature 409, 529-533, 2001
 A;Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.
 A;Reference number: A85480; MUID:21074935; PMID:11206551
 A;Accession: F83695
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-270 <STOP>
 A;Cross-references: GB:J03153; NID:9146865; PIDN:AAB59062.1; PID:9146867
 C;Sequence: Escherichia coli
 C;Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 19-Jan-2001
 C;Accession: B31877; D64663
 R;de Boer, P.A.J.; Crossley, R.E.; Rothfield, L.I.
 Cell 56, 641-649, 1989
 A;Title: A division inhibitor and a topological specificity factor coded for by the mini CCECD
 cell division inhibitor mind - *Escherichia coli*
 N;Alternate names: septum site-determining protein mind
 C;Species: *Escherichia coli*
 C;Accession: B31877
 R;de Boer, P.A.J.; Crossley, R.E.; Rothfield, L.I.
 Cell 56, 641-649, 1989
 A;Reference number: A31877; MUID:89136010
 A;Accession: B31877
 A;Molecule type: DNA
 A;Residues: 1-270 <DB>
 A;Cross-references: GB:J03153; NID:9146865; PIDN:AAB59062.1; PID:9146867
 R;Blattner, F.R.; Plunkett III, G.; Perna, N.T.; Burland, V.; Riley, M.; Cole, R.; Rose, D.J.; Mau, B.; Shao, Y.
 Science 277, 1453-1462, 1997
 A;Title: The complete genome sequence of *Escherichia coli* K-12.
 A;Reference number: A64720; MUID:9146617
 A;Accession: D64863
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-270 <BLAT>
 A;Cross-references: GB:AE000216; GB:U00096; NID:91787417; PIDN: AAC74259.1; PID:91787423;

RESULT 13
 A; Accession: C82136
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-276 <HEI>
 A; Cross-references: GB:AE004271; CR:AE003852; NID:99656490; PIDN:AAF95108.1; GSPDB:GN
 A; Experimental source: serogroup O1; strain N16961; biotype El Tor
 A; Genetics:
 A; Gene: VC1960
 A; Map Position: 1
 C; Superfamily: cell division inhibitor mIND

Query Match 26.3%; Score 468; DB 2; Length 276;
 Best Local Similarity 40.4%; Pred. No. 3.9e-30;
 Matches 112; Conservative 57; Mismatches 90; Indels 18; Gaps 7;

Qy 59 RIVVITSGKGKGKTTTANGLSARAYGFSVVAIDGLRLDGLLGLENRNYTCVE 118
 Db 9 RIVVITSGKGKGKTTTANGLSARAYGFSVVAIDGLRLDGLLGLENRNYTCVE 118
 Qy 119 VINGCDRLQALVRDKRWSNPFLCLTSKPRSKLPMGFGKALEWLDAKLTRPEGSPDFI 178
 Db 69 VINGCDRLQALVRDKRWSNPFLCLTSKPRSKLPMGFGKALEWLDAKLTRPEGSPDFI 178
 Qy 179 LIDCPAGIDAGLTATPAANEAVLYTPDITALDRDVRTELECDR-----DTK-- 230
 Db 124 TDCSPAGIDAGLTATPAANEAVLYTPDITALDRDVRTELECDR-----DTK-- 230
 Qy 231 MIVNRVRTDMIKGEDMMSYLDQEMGLSLLGVIPEDSEYVIRSTNRGFPLVNLKEPTLAG 290
 Db 184 LLTRTRYNPARYTQGEMMSVQDVEEILHVPVLGVIPESQAVLNASNQGPVIFDDQSD-AG 242
 Qy 291 LAFEQAAWRLV-EQDSMKAVVNEEPPKKRGFFSFFGG 326
 Db 243 QAYQDTVARLGEQEYERFL---TEAKKGFKRLFGG 276

RESULT 15
 A; Accession: B84968
 A; Status: site-determining protein Mind - Thermotoga maritima (strain MSB8)
 A; Molecule type: DNA
 A; Residues: 1-271 <ARN>
 A; Cross-references: GB:AE001824; PIDN:AAD69932.1; PID:9498245
 A; Experimental source: strain MSB8
 C; Genetics:
 A; Gene: TM1870
 C; Superfamily: cell division inhibitor mIND

Query Match 28.7%; Score 475.5; DB 2; Length 271;
 Best Local Similarity 40.9%; Pred. No. 9.5e-31;
 Matches 105; Conservative 47; Mismatches 68; Indels 37; Gaps 5;

Qy 60 RIVVITSGKGKGKTTTANGLSARAYGFSVVAIDGLRLDGLLGLENRNYTCVE 119
 Db 4 RIVVITSGKGKGKTTTANGLSARAYGFSVVAIDGLRLDGLLGLENRNYTCVE 119
 Qy 120 VINGCDRLQALVRDKRWSNPFLCLTSKPRSKLPMGFGKALEWLDAKLTRPEGSP--- 175
 Db 64 VNGKVSPQEALVKHMKLKNYL----PASQ-----IAKEMISPNDMK 103
 Qy 176 -----DFIDCPAGIDAGLTATPAANEAVLYTPDITALDRDVRTELECDG 225
 .Db 104 ATVKELPHEDVITIDSPAGIERGRNAVADPERVIVVTPDPLAISADRIVGLENFG 163
 Qy 226 IRD--TKMVNRVRTDMIKGEDMMSYLDQEMGLSLLGVIPEDSEVIRSTNRGFPLVNL 283
 Db 164 FSDERKINVINRFPHMVKRGEMLTDIKHTLSLEIATVIPSDEDIVASNTGIPVSLN 223
 Qy 284 KPPPLAGLAEQAWRL 300
 Db 224 GNSRIS-KNFENLARRI 239

RESULT 14
 C82136
 A; Accession: C82136
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-270 <STP>
 A; Cross-references: GB:AP000398; GSPDB:GN00144
 A; Experimental source: strain APs
 C; Genetics:
 A; Gene: BU326
 C; Superfamily: cell division inhibitor mIND

Query Match 27.8%; Score 460; DB 2; Length 270;
 Best Local Similarity 38.3%; Pred. No. 1.6e-29;
 Matches 106; Conservative 60; Mismatches 91; Indels 20; Gaps 5;

Qy 59 RIVVITSGKGKGKTTTANGLSARAYGFSVVAIDGLRLDGLLGLENRNYTCVE 118
 Db 3 RIVVITSGKGKGKTTTANGLSARAYGFSVVAIDGLRLDGLLGLENRNYTCVE 118
 Qy 119 VINGCDRLQALVRDKRWSNPFLCLTSKPRSKLPMGFGKTTIVIDFDGLRLDGLLGLENRNYTCVE 118
 Db 63 VIQGDTLQALVKHMKLKNYL----PASQ-----IAKEMISPNDMK 103
 Qy 177 FIIDCPAGIDAGLTATPAANEAVLYTPDITALDRDVRTELECDG 225
 Db 116 FTICDSPAGIEGTGALLAIYFAADEAITTNPVSVSDSRTLGISSKSKRAEKNTPK 175

RESULT 15
 A; Accession: C82136
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-270 <HEI>
 A; Cross-references: GB:AE02136
 A; Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
 A; Genetics:
 A; Gene: R.J.; Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; chardson, D.; Ermolaeva, M.D.; Vanathavan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F.; R.R. Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
 A; Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
 A; Reference number: A82035; MUID:20406833

QY 231 - -MIVNRVRTDMMIKGEDMMSSVLDYQEMGLSLLGVIPEDSEVIRSTNRGFLPLVLNKPPTL 288
Db 176 EYLLJTRYNPRVKGEMLSNTDVLDILQTPIGVIPEDQSVLRA\$NOGESTILDINSN- 234
QY 289 AGLAFAEQAAWRLEQDSMKAIVMVEEPKKRQFSFSG 325
Db 235 AGCAYSDTVNLGEE- -RHFRFIEBEKKSFLRLFG 269

Search completed: February 11, 2002, 13:33:03
Job time: 110 sec